AMENDMENTS TO THE SPECIFICATION

Please amend the specification at page 8, lines 9-30 of the application as filed according to the mark-ups below.

As mentioned above, polyphosphate can accumulate in all organisms in significant amounts and can be quantified directly by ^{31}P-NMR. Polyphosphate synthetase genes, for instance PHM genes of *Saccharomyces cerevisiae*, specifically PHM 1-4 genes placed downstream of the chosen gene and in-frame with it allow transcription to be quantified in real time. ~~The polyphosphate generated by this method has a mean length of up to 50 phosphate groups, within the detectable range by NMR.~~ Polyphosphates generated by this method have an average length of 50 phosphate groups. This size is within the limits of detection by NMR. The 10 mer is thought to show the highest sensitivity for ^{31}P-NMR. The polymer sizes can be confirmed by staining the cell contents with toluidine blue after polyacrylamide gel-electrophoresis. Importantly, NMR signals derived from polyphosphate can be independently quantified without interference from signals of nucleic acids. DNA sequences of PHM 1-5 genes and amino acid sequences of PHM 1-5 are shown by Seq. I.D. Nos. 1-10. As for the polyphosphate synthetases used, there is no particular restriction as long as the synthetases can generate polyphosphate intracellularly. PPK (polyphosphate kinase) derived from prokaryotic organisms, functional homologues, or orthlogues, other than PHM of the aforementioned *Saccharomyces cerevisiae* can be used.